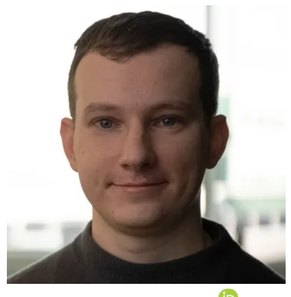
Multi-omic integration at the intersection of diet, metabolism, and gut microbiota

[1]Artur Sannikov, [2]Veera Houttu, [1]Ville Koistinen, [1]Topi Meuronen, [1]Sara Ferreira Rocha, [1]Jasmin Raita, [3]Leo Lahti,[1]Kati Hanhineva

[1]Department of Life Technologies, University of Turku, [2]Nutrition and Food Research Center, University of Turku, [3]Department of Computing, University of Turku



[2]arsann@utu.fi, 0000-0001-7765-123X

Github: artur-sannikov

Introduction

There is an urgent global need to increase the consumption of plant-based foods for human health and sustainable food production. Novel methods have emerged to manufacture protein-rich plant-based foods to achieve good nutritional and sensory properties, but their effects on human health, including microbiota, are not yet well studied.

Study design and goal

In the **Newplant** project, we conducted a clinical intervention with 37 participants, who followed three types of diet—whole unprocessed plant-based (e.g., canned beans), mildly processed (e.g., tofu), and refined (e.g., soy nuggets)—over five weeks (Figure 1). We collected metabolomic, metagenomic, clinical, and food frequency data to investigate links between the studied dietary patterns and biological changes. In this study, we aim to identify **patterns of co-variation between metagenomic and metabolomic profiles** to understand whether specific microbial taxa or metabolites show consistent shifts both within and across diets.

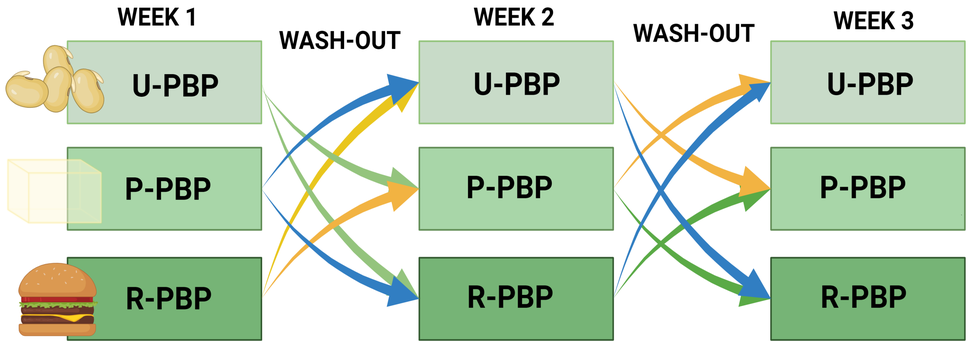


Fig. 1: Newplant clinical intervention design. The intervention was performed over 5 weeks. Volunteers eat their normal diets between the intervention diets to wash-out the diet effects. The samples were collected at the start and the end of each diet week.

Methods

We calculated the Shannon alpha-diversity of metagenomic profiles in two ways: first, by considering diversity for each of the three diet types regardless of time point, and second, by also considering timepoints. We then performed Wilcoxon paired tests for both approaches.

Results

In the pulled diets variant, we observed a statistically significant ($p < 0.05$) **decrease in alpha-diversity across all three diet groups**. The mean log-fold change values were similar among diets. However, the range of changes was greater in the whole unprocessed and mildly processed diets compared to the refined diet. Notably, the whole plant-based diet displayed more samples with higher log fold changes, whereas variability in the mildly processed diet was largely driven by a single sample (Figure 2). Additionally we demonstrate the correlations between identified metabolites and selected microbial genera (Figure 3) per each of the three diets. In the refined diet (Figure 3B), we observed a negative correlation between *Butyricicoccus* and p-cresol sulfate. **p-cresol sulfate** is a metabolite known to be invovled in chronic kidney disease.

Fig. 2: Alpha-diversity decreases across all diets

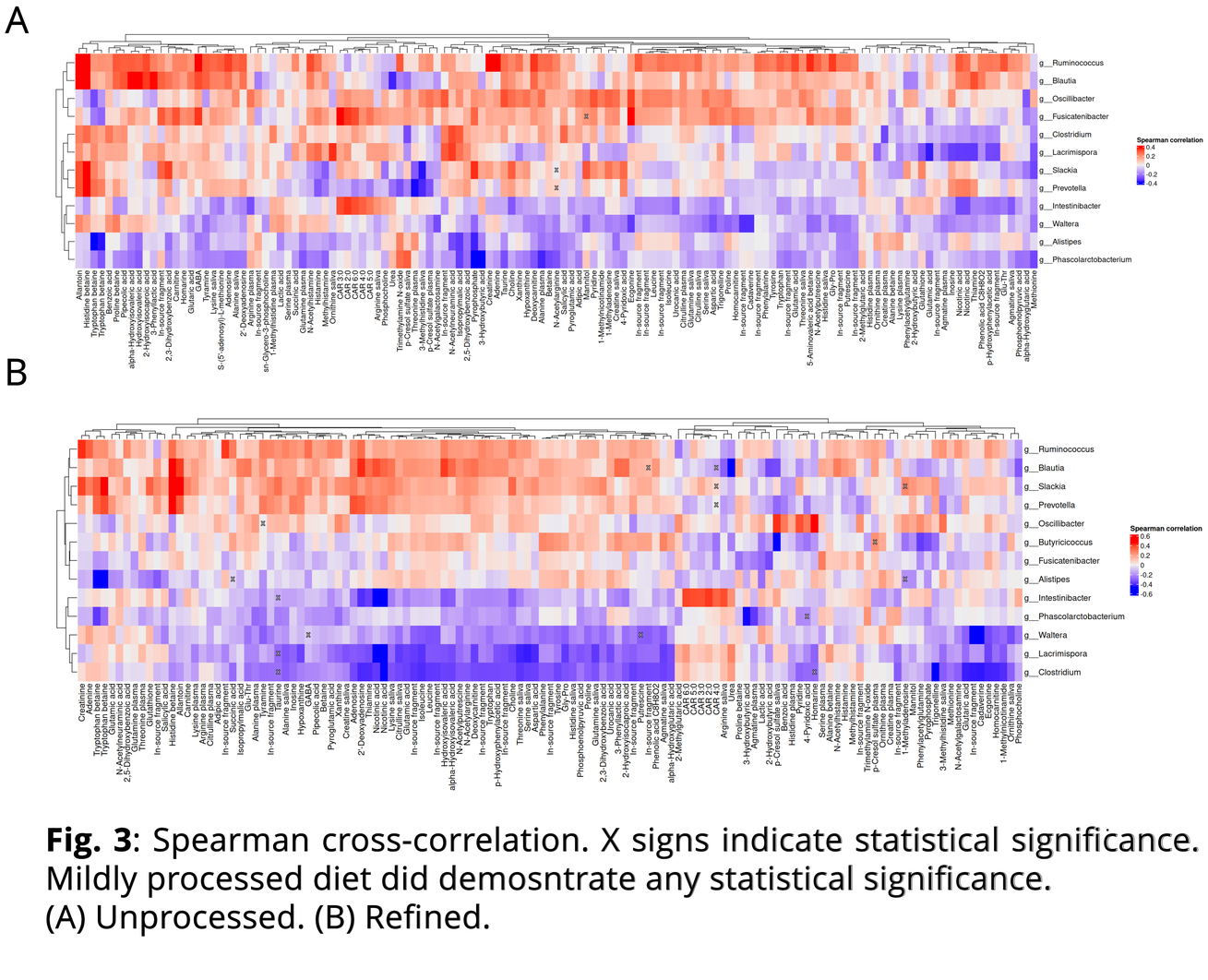


Fig. 3: Spearman cross-correlation. X signs indicate statistical significance. Mildly processed diet did demosntrate any statistical significance. (A) Unprocessed. (B) Refined.

Conclusions and future directions

In the **Newplant** study, we collected omic and clinical data to study how processing of plant-based protein-rich foods affects on circulating metabolites and gut microbiota. Alpha-diversity consistently decreased across all diets and time points. Future work will examine abundance shifts in individual taxa and metabolites and investigate co-variation among metagenomic, metabolomic, and clinical data to better understand health impacts of plant-based products.

Acknowledgements

We are grateful to Finnish Functional Genomics Centre at Biocity Turku for metagenomic sequencing. We also extend our thanks to all the developers of software that is being used in this study.